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EL591094879US

SEQUENCE LISTING

<110> Immunex Corporation

<120> NEW METALLO-PROTEINASE INHIBITOR IN FAMILY MEMBERS WITH
DIAN AND POLYPEPTIDES

<130> 04260.0093 00304

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<150> 60/116,670

<151> 1999-01-21

<150> 60/138,682

<151> 1999-06-14

<150> 60/155,798

<151> 1999-09-27

<160> 33

<170> PatentIn Ver. 2.1

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<211> 129

<212> DNA

<213> Homo sapiens

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<223> "n" at various positions throughout the sequence
may be any nucleotide

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<211> 469

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<223> "Xaa" at various positions throughout the sequence
may be any amino acid

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 35 40 45

Ala Pro Leu Cys His Leu Ser Gly Thr Val Leu Gln Gln Gly Thr Arg
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Val Gly Thr Ala Ala Leu Ser Ala Cys His Gly Leu Thr Gly Phe Phe
 65 70 75 80

Gln Leu Pro His Gly Asp Phe Phe Ile Glu Pro Val Lys Lys His Pro
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Leu Val Glu Gly Gly Tyr His Pro His Ile Val Tyr Arg Arg Gln Lys
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Val Pro Glu Thr Lys Glu Pro Thr Cys Gly Leu
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<211> 499

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<213> Homo sapiens

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 35 40 45

Leu Gly His Ala Val Gly Met Ser His Asp Glu Gln Tyr Cys Gln Cys
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Asn Cys Ser Tyr Ile Ser Phe Phe Lys His Ile Ser Ser Gly Ala Thr
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 Glu Tyr Cys Asp Gly Asn Ser Ser Ser Cys Pro Asn Asp Val Tyr Lys
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 Gln Asp Gly Thr Pro Cys Lys Tyr Glu Gly Arg Cys Phe Arg Lys Gly
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 Cys Arg Ser Arg Tyr Met Gln Cys Gln Ser Ile Phe Gly Pro Asp Ala
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 Glu Ser Ala Asn Ser Ile Cys Gly Arg Leu Gln Cys Ile Asn Val Glu
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 290 295 300
 Lys Pro Met Gly Ile Pro Asp Leu Gly Met Ile Asn Asp Gly Thr Ser
 305 310 315 320
 Cys Gly Glu Gly Arg Val Cys Phe Lys Lys Asn Cys Val Asn Ser Ser
 325 330 335
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 355 360 365
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 370 375 380
 Gly Leu Leu Arg Gly Ala Ile Pro Leu Ser Ile Trp Val Val Ser Ile
 385 390 395 400
 Ile Met Phe Arg Leu Ile Leu Leu Ile Leu Ser Val Val Phe Val Phe
 405 410 415
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Val Gln Glu Glu Ser Lys Thr Lys Thr Gly Gln Glu Glu Ser Glu Ala
450 455 460

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Gln Lys Lys

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<211> 2301

<212> DNA

<213> Homo sapiens

<400> 7

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<212> DNA

<213> Homo sapiens

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<211> 2346

<212> DNA

<213> Homo sapiens

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ctcctgaaga aagagcagtt tgggaatcag gtttgtgggt taagtgtatg tgaatagaa 540
tggcagatga ccccttatga gaataagggc aggtctaggc actttcctgg atccatataa 600
cagccaaagt acttggaaft gactctaact ttgtatcaaa gtaggatatg gtttgtgaac 660
aacaatcttt ctcaagtcac acatgatgcc attcttttga ctgggattat ggacacctac 720
tttcaagatg ttccgatgag qatacaactta aaggetcttg aagtatggac agattttaac 780
aaaatacgcg ttggatatcc agagtttagc gaagtttttag gcagatttgt aatatataaa 840
aaaagtgtat taaatgctcc cctgtcatca qatttggcac atttatatct tcaaaagaaa 900
tataatqatg cttcttcaatg qtcgtttgga aaagtgtgtt ctttagaata tcttgaatca 960
atgaatactt tactatatac aaatatcctt qccctgata ccttgcctgc tcatgaatca 1020

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```

attggaacttt getgtcatga ttgtcggttt cctccatctg gatacgtgtg taggcaggaa 1380
aaaaatgaat qtgaccttgc aaagtactgc qacgggaatt caagttcctg cccaaatgac 1440
atttataagc aggatggaac cctttcaaa tatgaaggcc gtgtgttctag gaagggggtg 1500
agatccagat atatgcagtg ccaaaacatt ttggacctg atgccatgga gactcctagt 1560
aagtgetatg atgcagttaa cttaataagt gatcaatttg qtaactgtga qattacagga 1620
attcgaaatt tttaaaagtg taaaagtga aattcaatat gtgcacappct acaagtata 1680
aattgttgaac ccatcctga ttgcacagag catacgaacta taatttctac tcatttagag 1740
gcagaaaaatc tcattgtctg gggcacagge tatcatctat ccatgaaacc catgggaata 1800
cctgacctag gtatgataaa tgatggcacc tctgtgtgag aaggccgggt atgtttttaa 1860
aaaaattggc tcaatagctc agtccctgcag tttgactgtt tgcctgagaa atgcaatacc 1920
cggggtgttt gcaacaacag aaaaaactgc cactgcatgt atgggtgggc acctccatto 1980
tgtgaggaag tggggtatgg aggaagcatt gacagtgggc ctccaggact gctcagaggg 2040
gegattccct cgtcaatttg ggttgtgtcc atcataatgt ttegccttat ttattaate 2100
ctttcagtg tttttgtgt tttccggcaa gtgataggaa accacttaaa acccaaacag 2160
gaaaaaatgc cactatccaa agcaaaaact gaacaggaag aatetaaaac aaaaactgta 2220
caggaagaat ctaaaacaaa aactggacag gaagaatctg aagcaaaaac tggacaggaa 2280
gaatctaaag caaacattga aagtaaacga cccaaagcaa agagtgtcaa gaaacaaaaa 2340
aagtaa 2346

```

<210> 12

<211> 766

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
  1              5              10              15

```

```

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
      20              25              30

```

```

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
      35              40              45

```

```

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
      50              55              60

```

```

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
      65              70              75              80

```

```

Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
      85              90              95

```

```

Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
      100              105              110

```

```

Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
      115              120              125

```

```

Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
      130              135              140

```

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
 180 185 190
 Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
 195 200 205
 Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
 210 215 220
 Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
 225 230 235 240
 Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
 245 250 255
 Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
 260 265 270
 Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
 275 280 285
 Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
 290 295 300
 Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
 305 310 315 320
 Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
 325 330 335
 Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
 340 345 350
 Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
 355 360 365
 Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
 370 375 380
 Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
 385 390 395 400
 Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
 405 410 415
 Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
 420 425 430
 Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
 435 440 445
 Leu Pro Ser Gly Leu Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu

Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
 485 490 495
 Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
 500 505 510
 Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
 515 520 525
 Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
 530 535 540
 Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
 545 550 555 560
 Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
 565 570 575
 Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
 580 585 590
 Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
 595 600 605
 Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
 610 615 620
 Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
 625 630 635 640
 His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
 645 650 655
 Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
 660 665 670
 Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
 675 680 685
 Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
 690 695 700
 Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
 705 710 715 720
 Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
 725 730 735
 Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Arg Gln Pro
 740 745 750
 Gln Leu Met Thr Ser Gln Ser Gln Pro Pro Val Thr Pro Ser
 755 760 765

213 - Homo sapiens

1400 - 14

Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
20 25 30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro
35 40 45

Pro Gly Trp Leu Ser Tyr Ile Leu Pro Phe Gly Gly Gln Lys His Ile
50 55 60

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
65 70 75 80

Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
85 90 95

Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
100 105 110

Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
115 120 125

Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
130 135 140

Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
145 150 155 160

Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
165 170 175

Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
180 185 190

Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
195 200 205

Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
210 215 220

Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
225 230 235 240

Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
245 250 255

Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
260 265 270

Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
 290 295 300
 Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
 305 310 315
 Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
 320 325 330
 Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Arg Cys Ser Gln Pro
 340 345 350
 Arg Cys Ile Met His Glu Gly Asn Pro Pro Ile Thr Lys Phe Ser Asn
 355 360 365
 Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
 370 375 380
 Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
 385 390 395 400
 Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
 405 410 415
 Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
 420 425 430
 Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
 435 440 445
 Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
 450 455 460
 Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
 465 470 475 480
 Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
 485 490 495
 Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
 500 505 510
 Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
 515 520 525
 Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
 530 535 540
 Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
 545 550 555 560
 Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
 565 570 575

Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
 634 639 644
 Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
 649 654 659
 Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
 664 669 674 679
 His Cys His Cys Asn Tyr Leu Trp Asp Pro Pro Asn Cys Leu Ile Lys
 684 689 694
 Gly Tyr Gly Gly Ser Val Asp Ser Gly Pro Pro Pro Lys Arg Lys Lys
 699 704 709
 Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
 714 719 724 729
 Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Pro Ile
 734 739 744 749
 Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Glu Glu Glu Lys
 754 759 764 769
 Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
 774 779 784 789
 Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
 794 799 804 809
 Gln Val Met Pro Ser Gln Ser Gln Pro Pro Gln Asn Leu Phe Leu Phe
 814 819 824 829
 Ser Phe Ser Ile Ser Asp Cys Val Leu Asn Phe Arg Leu Leu Tyr Leu
 834 839 844 849
 Gln Ala Thr
 854

<210> 14

<211> 820

<212> PPT

<213> Homo sapiens

<400> 14

Met Lys Met Leu Leu Leu Leu His Cys Leu Gly Val Phe Leu Ser Cys
 1 5 10 15

Ser Gly His Ile Gln Asp Glu His Pro Gln Tyr His Ser Pro Pro Asp
 20 25 30

Val Val Ile Pro Val Arg Ile Thr Gly Thr Thr Arg Gly Met Thr Pro

Ile His Ile Lys Val Lys Lys Leu Leu Phe Ser Lys His Leu Pro Val
 65 70 75 80
 Phe Thr Tyr Thr Asp Gln Gly Ala Ile Leu Glu Asp Gln Pro Phe Val
 85 90 95
 Gln Asn Asn Cys Tyr Tyr His Gly Tyr Val Glu Gly Asp Pro Glu Ser
 100 105 110
 Leu Val Ser Leu Ser Thr Cys Phe Gly Gly Phe Gln Gly Ile Leu Gln
 115 120 125
 Ile Asn Asp Phe Ala Tyr Glu Ile Lys Pro Leu Ala Phe Ser Thr Thr
 130 135 140
 Phe Glu His Leu Val Tyr Lys Met Asp Ser Glu Glu Lys Gln Phe Ser
 145 150 155 160
 Thr Met Arg Ser Gly Phe Met Gln Asn Glu Ile Thr Cys Arg Met Glu
 165 170 175
 Phe Glu Glu Ile Asp Asn Ser Thr Gln Lys Gln Ser Ser Tyr Val Gly
 180 185 190
 Trp Trp Ile His Phe Arg Ile Val Glu Ile Val Val Val Ile Asp Asn
 195 200 205
 Tyr Leu Tyr Ile Arg Tyr Glu Arg Asn Asp Ser Lys Leu Leu Glu Asp
 210 215 220
 Leu Tyr Val Ile Val Asn Ile Val Asp Ser Ile Leu Asp Val Ile Gly
 225 230 235 240
 Val Lys Val Leu Leu Phe Gly Leu Glu Ile Trp Thr Asn Lys Asn Leu
 245 250 255
 Ile Val Val Asp Asp Val Arg Lys Ser Val His Leu Tyr Cys Lys Trp
 260 265 270
 Lys Ser Glu Asn Ile Thr Pro Arg Met Gln His Asp Thr Ser His Leu
 275 280 285
 Phe Thr Thr Leu Gly Leu Arg Gly Leu Ser Gly Ile Gly Ala Phe Arg
 290 295 300
 Gly Met Cys Thr Pro His Arg Ser Cys Ala Ile Val Thr Phe Met Asn
 305 310 315 320
 Lys Thr Leu Gly Thr Phe Ser Ile Ala Val Ala His His Leu Gly His
 325 330 335
 Asn Leu Gly Met Asn His Asp Glu Asp Thr Cys Ala Cys Ser Gln Pro
 340 345 350

Cys Ser Tyr Gly Asp Phe Trp Glu Tyr Thr Val Glu Arg Thr Lys Cys
 370 375 380
 Leu Leu Glu Thr Val His Thr Lys Asp Ile Phe Asn Val Lys Arg Cys
 385 390 400
 Gly Asn Gly Val Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Pro Leu
 405 410 415
 Lys His Cys Ala Lys Asp Pro Cys Cys Leu Ser Asn Cys Thr Leu Thr
 420 425 430
 Asp Gly Ser Thr Cys Ala Phe Gly Leu Cys Cys Lys Asp Cys Lys Phe
 435 440 445
 Leu Pro Ser Gly Lys Val Cys Arg Lys Glu Val Asn Glu Cys Asp Leu
 450 455 460
 Pro Glu Trp Cys Asn Gly Thr Ser His Lys Cys Pro Asp Asp Phe Tyr
 465 470 475 480
 Val Glu Asp Gly Ile Pro Cys Lys Glu Arg Gly Tyr Cys Tyr Glu Lys
 485 490 495
 Ser Cys His Asp Arg Asn Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly
 500 505 510
 Ala Asn Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly
 515 520 525
 Asp Arg Val Gly His Cys Gly Ile Lys Asn Ala Thr Tyr Ile Lys Cys
 530 535 540
 Asn Ile Ser Asp Val Gln Cys Gly Arg Ile Gln Cys Glu Asn Val Thr
 545 550 555 560
 Glu Ile Pro Asn Met Ser Asp His Thr Thr Val His Trp Ala Arg Phe
 565 570 575
 Asn Asp Ile Met Cys Trp Ser Thr Asp Tyr His Leu Gly Met Lys Gly
 580 585 590
 Pro Asp Ile Gly Glu Val Lys Asp Gly Thr Glu Cys Gly Ile Asp His
 595 600 605
 Ile Cys Ile His Arg His Cys Val His Ile Thr Ile Leu Asn Ser Asn
 610 615 620
 Cys Ser Pro Ala Phe Cys Asn Lys Arg Gly Ile Cys Asn Asn Lys His
 625 630 635 640
 His Cys His Cys Asn Tyr Leu Trp Asp Pro Leu Asn Cys Leu Ile Lys
 645 650 655

Lys Lys Lys Phe Cys Tyr Leu Cys Ile Leu Leu Leu Ile Val Leu Phe
675 680 685

Ile Leu Leu Cys Cys Leu Tyr Arg Leu Cys Lys Lys Ser Lys Phe Ile
690 695 700

Lys Lys Gln Gln Asp Val Gln Thr Pro Ser Ala Lys Gln Gln Gln Lys
705 710 715 720

Ile Gln Arg Arg Pro His Glu Leu Pro Pro Gln Ser Gln Pro Trp Val
725 730 735

Met Pro Ser Gln Ser Gln Pro Pro Val Thr Pro Ser Gln Ser His Pro
740 745 750

Arg Val Met Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser Gln Ser
755 760 765

His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Met Pro Ser
770 775 780

Gln Ser His Pro Gln Leu Thr Pro Ser Gln Ser Gln Pro Pro Val Thr
785 790 795 800

Pro Ser Gln Arg Gln Pro Gln Leu Met Pro Ser Gln Ser Gln Pro Pro
805 810 815

Val Thr Pro Ser
820

<210> 15

<211> 790

<212> PRT

<213> Homo sapiens

<400> 15

Met Arg Ser Val Gln Ile Phe Leu Ser Gln Cys Arg Leu Leu Leu Leu
1 5 10 15

Leu Val Pro Thr Met Leu Leu Lys Ser Leu Gly Glu Asp Val Ile Phe
20 25 30

His Pro Glu Gly Glu Phe Asp Ser Tyr Glu Val Thr Ile Pro Glu Lys
35 40 45

Leu Ser Phe Arg Gly Gln Val Gln Gly Val Val Ser Pro Val Ser Tyr
50 55 60

Leu Leu Gln Leu Lys Gly Lys Lys His Val Leu His Leu Trp Pro Lys
65 70 75 80

Arg Leu Leu Leu Pro Arg His Leu Arg Val Phe Ser Phe Thr Gln His

Met Gly Ser Val Lys Glu Ser Leu Asp Ser Lys Ala Thr Ile Ser Thr
115 120 125

Cys Met Gly Gly Leu Arg Gly Val Phe Asn Ile Asp Ala Lys His Tyr
130 135 140

Gln Ile Glu Pro Leu Lys Ala Ser Pro Ser Phe Glu His Val Val Tyr
145 150 155 160

Leu Leu Lys Lys Glu Gln Phe Gly Asn Gln Val Cys Gly Leu Ser Asp
165 170 175

Asp Glu Ile Glu Trp Gln Met Ala Pro Tyr Glu Asn Lys Ala Arg Leu
180 185 190

Arg Asp Phe Pro Gly Ser Tyr Lys His Pro Lys Tyr Leu Glu Leu Ile
195 200 205

Leu Leu Phe Asp Gln Ser Arg Tyr Arg Phe Val Asn Asn Asn Leu Ser
210 215 220

Gln Val Ile His Asp Ala Ile Leu Leu Thr Gly Ile Met Asp Thr Tyr
225 230 235 240

Phe Gln Asp Val Arg Met Arg Ile His Leu Lys Ala Leu Glu Val Trp
245 250 255

Thr Asp Phe Asn Lys Ile Arg Val Gly Tyr Pro Glu Leu Ala Glu Val
260 265 270

Leu Gly Arg Phe Val Ile Tyr Lys Lys Ser Val Leu Asn Ala Arg Leu
275 280 285

Ser Ser Asp Trp Ala His Leu Tyr Leu Gln Arg Lys Tyr Asn Asp Ala
290 295 300

Leu Ala Trp Ser Phe Gly Lys Val Cys Ser Leu Glu Tyr Ala Gly Ser
305 310 315 320

Val Ser Thr Leu Leu Asp Thr Asn Ile Leu Ala Pro Ala Thr Trp Ser
325 330 335

Ala His Glu Leu Gly His Ala Val Gly Met Ser His Asp Glu Gln Tyr
340 345 350

Cys Gln Cys Arg Gly Ala Pro Asn Cys Ile Met Gly Ser Gly Arg Thr
355 360 365

Gly Phe Ser Asn Cys Ser Tyr Ile Ser Phe Phe Lys His Ile Ser Ser
370 375 380

Gly Ala Thr Cys Leu Asn Asn Ile Pro Gly Leu Gly Tyr Val Leu Lys
385 390 395 400

Ser Thr Glu Glu Cys Gln Lys Asp Arg Cys Cys Gln Ser Asn Cys Lys
 410 425 430
 Leu Gln Pro Gly Ala Asn Cys Ser Ile Gly Leu Cys Cys His Asp Cys
 435 440 445
 Arg Phe Arg Pro Ser Gly Tyr Val Cys Arg Gln Glu Gly Asn Gln Cys
 450 455 460
 Asp Leu Ala Glu Tyr Cys Asp Gly Asn Ser Ser Ser Cys Pro Asn Asp
 465 470 475 480
 Val Tyr Lys Gln Asp Gly Thr Pro Cys Lys Tyr Glu Gly Arg Cys Phe
 485 490 495
 Arg Lys Gly Cys Arg Ser Arg Tyr Met Gln Cys Gln Ser Ile Phe Gly
 500 505 510
 Pro Asp Ala Met Glu Ala Pro Ser Glu Cys Tyr Asp Ala Val Asn Leu
 515 520 525
 Ile Gly Asp Gln Phe Gly Asn Cys Glu Ile Thr Gly Ile Arg Asn Phe
 530 535 540
 Lys Lys Cys Glu Ser Ala Asn Ser Ile Cys Gly Arg Leu Gln Cys Ile
 545 550 555 560
 Asn Val Glu Thr Ile Pro Asp Leu Pro Glu His Thr Thr Ile Ile Ser
 565 570 575
 Thr His Leu Gln Ala Glu Asn Leu Met Cys Trp Gly Thr Gly Tyr His
 580 585 590
 Leu Ser Met Lys Pro Met Gly Ile Pro Asp Leu Gly Met Ile Asn Asp
 595 600 605
 Gly Thr Ser Cys Gly Glu Gly Arg Val Cys Phe Lys Lys Asn Cys Val
 610 615 620
 Asn Ser Ser Val Leu Gln Phe Asp Cys Leu Pro Glu Lys Cys Asn Thr
 625 630 635 640
 Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys Met Tyr Gly Trp
 645 650 655
 Ala Pro Pro Phe Cys Glu Glu Val Gly Tyr Gly Gly Ser Ile Asp Ser
 660 665 670
 Gly Pro Pro Gly Leu Leu Arg Gly Ala Ile Pro Ser Ser Ile Trp Val
 675 680 685
 Val Ser Ile Ile Met Phe Arg Leu Ile Leu Leu Ile Leu Ser Val Val
 690 695 700

Gln Lys Met Pro Leu Ser Lys Ala Lys Thr Gln Gln Glu Glu Ser Lys
715 730 745

Thr Lys Thr Val Gln Glu Glu Ser Lys Thr Lys Thr Gly Gln Glu Glu
750 765 780

Ser Gln Ala Lys Thr Gly Gln Glu Gln Ser Lys Ala Lys Thr Gly Gln
785 800 815

Glu Glu Ser Lys Ala Asn Ile Glu Ser Lys Arg Pro Lys Ala Lys Ser
770 775 780

Val Lys Lys Gln Lys Lys
785 790

<210> 16

<211> 781

<212> PRT

<213> Homo sapiens

<400> 16

Met Arg Ser Val Gln Ile Phe Leu Ser Gln Cys Arg Leu Leu Leu Leu
1 5 10 15

Leu Val Pro Thr Met Leu Leu Lys Ser Leu Gly Glu Asp Val Ile Phe
20 25 30

His Pro Glu Gly Glu Phe Asp Ser Tyr Glu Val Thr Ile Pro Glu Lys
35 40 45

Leu Ser Phe Arg Gly Glu Val Gln Gly Val Val Ser Pro Val Ser Tyr
50 55 60

Leu Leu Gln Leu Lys Gly Lys Lys His Val Leu His Leu Trp Pro Lys
65 70 75 80

Arg Leu Leu Leu Pro Arg His Leu Arg Val Phe Ser Phe Thr Glu His
85 90 95

Gly Glu Leu Leu Glu Asp His Pro Tyr Ile Pro Lys Asp Cys Asn Tyr
100 105 110

Met Gly Ser Val Lys Glu Ser Leu Asp Ser Lys Ala Thr Ile Ser Thr
115 120 125

Cys Met Gly Gly Leu Arg Gly Val Phe Asn Ile Asp Ala Lys His Tyr
130 135 140

Gln Ile Glu Pro Leu Lys Ala Ser Pro Ser Phe Glu His Val Val Tyr
145 150 155 160

Leu Leu Lys Leu Glu Gln Phe Gly Asn Gln Val Cys Gly Leu Ser Asp

Arg Asp Phe Pro Gly Ser Tyr Lys His Pro Lys Tyr Leu Glu Leu Ile
 195 200 205
 Leu Leu Phe Asp Gln Ser Arg Tyr Arg Phe Val Asn Asn Asn Leu Ser
 210 215 220
 Gln Val Ile His Asp Ala Ile Leu Leu Thr Gly Ile Met Asp Thr Tyr
 225 230 235 240
 Phe Gln Asp Val Arg Met Arg Ile His Leu Lys Ala Leu Glu Val Trp
 245 250 255
 Thr Asp Phe Asn Lys Ile Arg Val Gly Tyr Pro Glu Leu Ala Glu Val
 260 265 270
 Leu Gly Arg Phe Val Ile Tyr Lys Lys Ser Val Leu Asn Ala Arg Leu
 275 280 285
 Ser Ser Asp Trp Ala His Leu Tyr Leu Gln Arg Lys Tyr Asn Asp Ala
 290 295 300
 Leu Ala Trp Ser Phe Gly Lys Val Cys Ser Leu Glu Tyr Ala Gly Ser
 305 310 315 320
 Val Ser Thr Leu Leu Asp Thr Asn Ile Leu Ala Pro Ala Thr Trp Pro
 325 330 335
 Ala His Glu Leu Gly His Ala Val Gly Met Ser His Asp Glu Gln Tyr
 340 345 350
 Cys Gln Cys Arg Gly Arg Leu Asn Cys Ile Met Gly Ser Gly Arg Thr
 355 360 365
 Gly Phe Ser Asn Cys Ser Tyr Ile Ser Phe Phe Lys His Ile Ser Ser
 370 375 380
 Gly Ala Thr Cys Leu Asn Asn Ile Pro Gly Leu Gly Tyr Val Leu Lys
 385 390 395 400
 Arg Cys Gly Asn Lys Ile Val Glu Asp Asn Glu Glu Cys Asp Cys Gly
 405 410 415
 Ser Thr Glu Glu Cys Gln Lys Asp Arg Cys Cys Gln Ser Asn Cys Lys
 420 425 430
 Leu Gln Pro Gly Ala Asn Cys Ser Ile Gly Leu Cys Tyr His Asp Cys
 435 440 445
 Arg Phe Arg Pro Ser Gly Tyr Val Cys Arg Gln Glu Gly Asn Glu Cys
 450 455 460
 Asp Leu Ala Glu Tyr Cys Asp Gly Asn Ser Leu Leu Cys Pro Asn Asn
 465 470 475 480

Arg Lys Gly Cys Arg Ser Arg Tyr Met Gln Cys Gln Ser Ile Phe Gly
 500 505 510
 Pro Asp Ala Met Glu Ala Pro Ser Gln Cys Tyr Asp Ala Val Asn Leu
 515 520 525
 Ile Gly Asp Gln Phe Gly Asn Cys Glu Ile Thr Gly Ile Arg Asn Phe
 530 535 540
 Lys Lys Cys Glu Ser Ala Asn Ser Ile Cys Gly Arg Leu Gln Cys Ile
 545 550 555 560
 Asn Val Glu Thr Ile Pro Asp Leu Pro Glu His Thr Thr Ile Ile Ser
 565 570 575
 Thr His Leu Gln Ala Glu Asn Leu Met Cys Trp Gly Thr Gly Tyr His
 580 585 590
 Leu Ser Met Lys Pro Met Gly Ile Pro Asp Leu Gly Met Ile Asn Asp
 595 600 605
 Gly Thr Ser Cys Gly Glu Gly Arg Val Cys Phe Lys Lys Asn Cys Val
 610 615 620
 Asn Ser Ser Val Leu Gln Phe Asp Cys Leu Pro Glu Lys Cys Asn Thr
 625 630 635 640
 Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys Met Tyr Gly Trp
 645 650 655
 Ala Pro Pro Phe Cys Glu Glu Val Gly Tyr Gly Gly Ser Ile Asp Ser
 660 665 670
 Gly Pro Pro Gly Leu Leu Arg Gly Ala Ile Pro Ser Ser Ile Trp Val
 675 680 685
 Val Ser Ile Ile Met Phe Arg Leu Ile Leu Leu Ile Leu Ser Val Val
 690 695 700
 Phe Val Phe Phe Arg Gln Val Ile Gly Asn His Leu Lys Pro Lys Gln
 705 710 715 720
 Glu Lys Met Pro Leu Ser Lys Ala Lys Thr Glu Gln Glu Glu Ser Lys
 725 730 735
 Thr Lys Thr Val Gln Glu Glu Ser Lys Thr Lys Thr Gly Gln Glu Glu
 740 745 750
 Ser Glu Ala Lys Thr Gly Gln Glu Glu Ser Lys Ala Asn Ile Glu Ser
 755 760 765
 Lys Arg Pro Lys Ala Lys Ser Val Lys Lys Gln Lys Lys
 770 775 780

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 17

caactaactg gttcattct ttg

22

<210> 18

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 18

caaatactgc aagtgagaact tgc

23

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 19

tgcacaacta cgtgtggtgt accc

24

<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 20

gagcaata caattatata ttatcc

25

<210> 21

<211> 21

<212> DNA

<213> Artificial Sequence

<400> 21
aattgatgctc ttgatgctc a 21

<210> 21
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 22
ctttcacgga gcccatgtag ttgcag 26

<210> 23
<211> 26
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 23
tgaaggagaa aacgcgcaga tgcagg 26

<210> 24
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 24
tcgataatgc atgaaggcaa cccacc 26

<210> 25
<211> 26
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<220>
<223> Description of Artificial Sequence: primer

<400> 25
caggttcac ttgcctatt ttgcag 26

<220>

<223> Description of Artificial Sequence: primer

<400> 26

gactctgcat ctatctcttct

17

<210> 27

<211> 21

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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gacactctttt gctttggggtc g

21

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide
fragment

<400> 28

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

<210> 29

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide
fragment

<400> 29

Pro Asp Val Ala Ser Leu Ala His Gln Val Gln Ala Leu Gln Asp Gln

1

6

16

25

Val Gln His Leu Gln Ala Ala His Ser Gln Tyr

20

29

<210> 30

<211> 33

<220>

<223> Description of Artificial Sequence: peptide fragment

<400> 30

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

Arg

<210> 31

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide fragment

<220>

<223> "Xaa" at various positions throughout the sequence may be any amino acid

<400> 31

His Glu Xaa Xaa His Xaa Xaa Gly Xaa Xaa His Asp
1 5 10

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide fragment

<400> 32

Ser Gln Ser Gln Pro Pro Leu Met Pro
1 5

<210> 33

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

1400-33

Gln Gln Gln Ser Lys Xaa Lys Thr Gly

1

5